

SEQUENCE LISTING

<110> JURECIC, ROLAND
NACHTMAN, RONALD

<120> HEPP, A NOVEL GENE WITH A ROLE IN HEMATOPOIETIC AND NEURAL
DEVELOPMENT

<130> 39532-176599

<150> US 60/268,923

<151> 2001-02-16

<160> 11

<170> PatentIn version 3.0

<210> 1

<211> 2082

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (191)..(901)

<400> 1

```

ccccgcgtcg gtcttccacc tcacctttcg agctggccgc cgcttgctgt gcgcagtttc      60
gggggactgg accttccctg gcttttagca gcgccgagcg ccatggcgac cctttgctgg      120
gcaggtgacc gattccgggt gcccaagga gctggcgtgg gtctgccttg cagccgcccg      180
cctggacagg atg ttt gct aga ggg ctg aag agg aaa tat ggt gac cag      229
          Met Phe Ala Arg Gly Leu Lys Arg Lys Tyr Gly Asp Gln
          1              5              10

gaa gaa gga gta gag ggt ttt ggc act gtc cct tcc tat agc ctg cag      277
Glu Glu Gly Val Glu Gly Phe Gly Thr Val Pro Ser Tyr Ser Leu Gln
          15              20              25

cga cag tca ctc ctg gac atg tcc ctt gtc aag ctc cag ctc tgt cac      325
Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys His
          30              35              40              45

atg cta gtg gag ccc aat ctc tgc cgc tcg gtc ctc atc gcc aac aca      373
Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn Thr
          50              55              60

gtc cgg cag atc cag gag gaa atg agc cag gat ggt gtg tgg cat ggg      421
Val Arg Gln Ile Gln Glu Glu Met Ser Gln Asp Gly Val Trp His Gly
          65              70              75

atg gca ccc cag aat gta gat cgg gca cca gtt gaa cgc ctg gtg tcc      469
Met Ala Pro Gln Asn Val Asp Arg Ala Pro Val Glu Arg Leu Val Ser
          80              85              90

```

aca gag atc ctg tgt cgt aca gtg agg gga gct gag gaa gag cac cct 517
 Thr Glu Ile Leu Cys Arg Thr Val Arg Gly Ala Glu Glu Glu His Pro
 95 100 105

gct cct gaa ctg gaa gat gct ccc ttg caa aac tcg gtt tcc gag ctc 565
 Ala Pro Glu Leu Glu Asp Ala Pro Leu Gln Asn Ser Val Ser Glu Leu
 110 115 120 125

ccc atc gtt ggc tca gca cca ggg caa agg aac cct cag agc agc ctc 613
 Pro Ile Val Gly Ser Ala Pro Gly Gln Arg Asn Pro Gln Ser Ser Leu
 130 135 140

tgg gag atg gac agc cca caa gaa aac agg gga agc ttt cag aag tca 661
 Trp Glu Met Asp Ser Pro Gln Glu Asn Arg Gly Ser Phe Gln Lys Ser
 145 150 155

ctg gac cag ata ttt gag acc ctg gag aac aaa aac tcc agt tca gtg 709
 Leu Asp Gln Ile Phe Glu Thr Leu Glu Asn Lys Asn Ser Ser Ser Val
 160 165 170

gag gaa ctc ttc tca gat gtg gac agc tcc tac tat gac ctg gac aca 757
 Glu Glu Leu Phe Ser Asp Val Asp Ser Ser Tyr Tyr Asp Leu Asp Thr
 175 180 185

gtg cta aca gga atg atg agt ggg acc aag tcc agt ctc tgc aat ggc 805
 Val Leu Thr Gly Met Met Ser Gly Thr Lys Ser Ser Leu Cys Asn Gly
 190 195 200 205

ctt gag ggc ttt gct gca gcc acc cct cct ccc agt tcc act tgc aag 853
 Leu Glu Gly Phe Ala Ala Ala Thr Pro Pro Pro Ser Ser Thr Cys Lys
 210 215 220

tct gac ctg gct gag ctg gac cat gtg gta gag att ctg gtg gag acc 901
 Ser Asp Leu Ala Glu Leu Asp His Val Val Glu Ile Leu Val Glu Thr
 225 230 235

tgagaggcca cccagtgagg ctaaggggtga ggccaccagt ccccatggag ctcacgtgtg 961

ttgtgacca gagacagata agcacttgct ctaagagggg ctctggctct tgagctcatt 1021

atccttttgt gtgacattgg actcactgtg gaggatgggtg tgtcacagct atgtctagtc 1081

tattttcaat tagataggtg aactttctaa aattaagttt tatatgtttt tgggcaatat 1141

tttgtcttaa gatataatttt ttaaactttt tatacttttag atttttttca gctattttct 1201

taaaagtata ttttttctac aaacatcctc tgctgtctaca ttagaaacat ttataacct 1261

aatacgattg gtgtgtcatt ttaaagggtt aaatagaaaa cttcttttgt tactgagtct 1321

ctacactccc aaggcaactg taaatgtagc cggccgggtg tttacatgag aggctccagt 1381

atgggtctaca ttctagtaga gcttgaaaag aaccatgcac agctccactg cccctcact 1441

gggtctgctc tggcggatcg gagctctctt cctagccccg tgtgcaggat ggctttatct 1501

atgcctatctt atatgtaaat gccactgaaa gctaagggtct tactcctgga aatcccaaca 1561

ccagttcttc agggactgct gtgaggcagt gccttatgca ggtcttgtcc ttggccatca 1621
 ctgtctgggtt cccagcccag cacatgtgac atgaggacat gacatgcccg aaccacccag 1681
 caccacatgc tccatgtcaa gtgtgtacgt ggagaccact ggctcccagg cctgtgtctca 1741
 gagaggggtgt gcagtcctac gtgtgctggg ggggacgacg gtgacctgtg cttgcttgct 1801
 tttaaaatgg tgcttggacg ttttaaggtt aaaaacaatc cgactccata tgatttaggg 1861
 ctccctccacc ctgggggtggc ccctatgctg tctgcttgga tctcaaagtc ttgggtactcg 1921
 gcactgtcag actccacccc atgtatcctt tttgtttctc ttgtgctttt tttggacttc 1981
 ccaacctgag cctaagggtt tattttatat gtgcttcaat atcaacaatg taaacctcac 2041
 tttattaaaa gtatccagca aatggaaaaa aaaaaaaaaa a 2082

<210> 2
 <211> 237
 <212> PRT
 <213> Mus musculus

<400> 2

Met Phe Ala Arg Gly Leu Lys Arg Lys Tyr Gly Asp Gln Glu Glu Gly
 1 5 10 15

Val Glu Gly Phe Gly Thr Val Pro Ser Tyr Ser Leu Gln Arg Gln Ser
 20 25 30

Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys His Met Leu Val
 35 40 45

Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn Thr Val Arg Gln
 50 55 60

Ile Gln Glu Glu Met Ser Gln Asp Gly Val Trp His Gly Met Ala Pro
 65 70 75 80

Gln Asn Val Asp Arg Ala Pro Val Glu Arg Leu Val Ser Thr Glu Ile
 85 90 95

Leu Cys Arg Thr Val Arg Gly Ala Glu Glu Glu His Pro Ala Pro Glu
 100 105 110

Leu Glu Asp Ala Pro Leu Gln Asn Ser Val Ser Glu Leu Pro Ile Val
 115 120 125

Gly Ser Ala Pro Gly Gln Arg Asn Pro Gln Ser Ser Leu Trp Glu Met
130 135 140

Asp Ser Pro Gln Glu Asn Arg Gly Ser Phe Gln Lys Ser Leu Asp Gln
145 150 155 160

Ile Phe Glu Thr Leu Glu Asn Lys Asn Ser Ser Ser Val Glu Glu Leu
165 170 175

Phe Ser Asp Val Asp Ser Ser Tyr Tyr Asp Leu Asp Thr Val Leu Thr
180 185 190

Gly Met Met Ser Gly Thr Lys Ser Ser Leu Cys Asn Gly Leu Glu Gly
195 200 205

Phe Ala Ala Ala Thr Pro Pro Pro Ser Ser Thr Cys Lys Ser Asp Leu
210 215 220

Ala Glu Leu Asp His Val Val Glu Ile Leu Val Glu Thr
225 230 235

<210> 3
<211> 2082
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(797)

<400> 3
gggaagctgg cggcacagcc gtggcgcttg gctgagcaga ggacccggcg ggcggcctcg 60

cgggtcagga caca atg ttt gca cga gga ctg aag agg aaa tgt gtt ggc 110
Met Phe Ala Arg Gly Leu Lys Arg Lys Cys Val Gly
1 5 10

cac gag gaa gac gtg gag gga gcc ctg gcc ggc ttg aag aca gtg tcc 158
His Glu Glu Asp Val Glu Gly Ala Leu Ala Gly Leu Lys Thr Val Ser
15 20 25

tca tac agc ctg cag cgg cag tcg ctc ctg gac atg tct ctg gtg aag 206
Ser Tyr Ser Leu Gln Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys
30 35 40

ttg cag ctt tgc cac atg ctt gtg gag ccc aac ctg tgc cgc tca gtc 254
Leu Gln Leu Cys His Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val
45 50 55 60

ctc att gcc aac acg gtc cgg cag atc caa gag gag atg acg cag gat 302
 Leu Ile Ala Asn Thr Val Arg Gln Ile Gln Glu Glu Met Thr Gln Asp
 65 70 75

ggg acg tgg cgc aca gtg gca ccc cag gct gca gag cgg gcg ccg ctc 350
 Gly Thr Trp Arg Thr Val Ala Pro Gln Ala Ala Glu Arg Ala Pro Leu
 80 85 90

gac cgc ttg gtc tcc acg gag atc ctg tgc cgt gca gcg tgg ggg caa 398
 Asp Arg Leu Val Ser Thr Glu Ile Leu Cys Arg Ala Ala Trp Gly Gln
 95 100 105

gag ggg gca cat cct gct cct ggc ttg ggg gac ggc cac aca cag ggt 446
 Glu Gly Ala His Pro Ala Pro Gly Leu Gly Asp Gly His Thr Gln Gly
 110 115 120

cca gtt tct gac ctt tgc cca gtc acc tca gca cag gca cca agg cac 494
 Pro Val Ser Asp Leu Cys Pro Val Thr Ser Ala Gln Ala Pro Arg His
 125 130 135 140

ctg cag agc agc gcc tgg gag atg gat ggc cct cga gaa aac aga gga 542
 Leu Gln Ser Ser Ala Trp Glu Met Asp Gly Pro Arg Glu Asn Arg Gly
 145 150 155

agc ttt cac aag tca ctt gat cag ata ttt gaa acg ctg gag act aaa 590
 Ser Phe His Lys Ser Leu Asp Gln Ile Phe Glu Thr Leu Glu Thr Lys
 160 165 170

aac ccc agc tgc atg gaa gag ctg ttc tca gac gtg gac agc ccc tac 638
 Asn Pro Ser Cys Met Glu Glu Leu Phe Ser Asp Val Asp Ser Pro Tyr
 175 180 185

tac gac ctg gac aca gta ctg aca ggc atg atg ggg ggt gcc agg ccg 686
 Tyr Asp Leu Asp Thr Val Leu Thr Gly Met Met Gly Gly Ala Arg Pro
 190 195 200

ggc ccc tgc gaa ggg ctc gag ggc ttg gct ccg gcc acc cca ggc cct 734
 Gly Pro Cys Glu Gly Leu Glu Gly Leu Ala Pro Ala Thr Pro Gly Pro
 205 210 215 220

agc tcc agc tgc aag tcc gac ctg ggc gag ctg gac cac gtg gtg gag 782
 Ser Ser Ser Cys Lys Ser Asp Leu Gly Glu Leu Asp His Val Val Glu
 225 230 235

atc ctg gtg gag acc tgagcaggag ccttgagtgc tcacagccgc ctctgacgca 837
 Ile Leu Val Glu Thr
 240

ttgacacgtg agcactggct cccacggagg gtgcgcctgc cgccagcggc ccagccttgc 897

tgcctgtct gctgattctg agaaatccca gaacagccca ttaccagtgg ggctgcagcc 957

ctaggcccgt cccactcacc tccccctgt ggagcgccag gcagaggctg ttctggaagg 1017

cttcttgtct tctgacgtcc ccacagccct gggcccctcg tgtctctttg tgtccccac 1077

tgttagaggac ggtgagccgc agctgcatca acctcctttt acctttagat aggtgaatth 1137
 ttacaattca gttttacatg ttttgggcag tattttgtct taagatatat tttttaaact 1197
 ttttatacct tatctcttta gattttttca gctattttct taaaagtata ttttttctat 1257
 aaacatcctt tgctgctaca ttagaacttt tatagcctaa acaattgcag ttggtgtgth 1317
 tcattttttt aagggtttaa taagggtttt ttgttttgth ttgttttttg cagtgcagat 1377
 cactacagtc tcagtcaaca gtgtgaatgt atcatgtttt actttaaatg tgtgtgtgat 1437
 acttcttcat tatgtcctgc gctgcagtga gacctgggtg aaaatcagga gccgcacaca 1497
 gccacatctt cctagaccta agagtaaatt atggaggatt ttatttatgt ctatttatat 1557
 gtaaagtca ttgaagacaa aggtcaaata tttgtctgth tgtagatcac aggcaccagt 1617
 tggctctcag ggacctcata gcccctcggg ggtgccttct caaggcagtg ttcctggagg 1677
 ctcccatcag ggtcagccca tgcacctgcc ctgggtgagg aagtagcatt gctgctggat 1737
 gagaaacgcc tgcgctgctc tgtagactg gtgctgaaac aaaagggtta ggctagggtg 1797
 aagtctagaa tgaaagaaat ctgaatccat gtcattcata accccttgat ctgtagtgth 1857
 atgggtgctg ccgcaggcag ggagtgcgt ggggggtgct gcagccttcc actcctgcc 1917
 cgctcacc ccatgctcc ctgtttctca tgccttctct aacttctca ccccttaacc 1977
 aaaaagggtg tttttctttt gtgcatatag ccattcttaa atatcagtga tgtaaacctc 2037
 actttattaa aaaattatcc agcaaaaaaa aaaaaaaaaa aaaaa 2082

<210> 4
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Phe Ala Arg Gly Leu Lys Arg Lys Cys Val Gly His Glu Glu Asp
 1 5 10 15

Val Glu Gly Ala Leu Ala Gly Leu Lys Thr Val Ser Ser Tyr Ser Leu
 20 25 30

Gln Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys
 35 40 45

His Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn
 50 55 60

Thr Val Arg Gln Ile Gln Glu Glu Met Thr Gln Asp Gly Thr Trp Arg
65 70 75 80

Thr Val Ala Pro Gln Ala Ala Glu Arg Ala Pro Leu Asp Arg Leu Val
85 90 95

Ser Thr Glu Ile Leu Cys Arg Ala Ala Trp Gly Gln Glu Gly Ala His
100 105 110

Pro Ala Pro Gly Leu Gly Asp Gly His Thr Gln Gly Pro Val Ser Asp
115 120 125

Leu Cys Pro Val Thr Ser Ala Gln Ala Pro Arg His Leu Gln Ser Ser
130 135 140

Ala Trp Glu Met Asp Gly Pro Arg Glu Asn Arg Gly Ser Phe His Lys
145 150 155 160

Ser Leu Asp Gln Ile Phe Glu Thr Leu Glu Thr Lys Asn Pro Ser Cys
165 170 175

Met Glu Glu Leu Phe Ser Asp Val Asp Ser Pro Tyr Tyr Asp Leu Asp
180 185 190

Thr Val Leu Thr Gly Met Met Gly Gly Ala Arg Pro Gly Pro Cys Glu
195 200 205

Gly Leu Glu Gly Leu Ala Pro Ala Thr Pro Gly Pro Ser Ser Ser Cys
210 215 220

Lys Ser Asp Leu Gly Glu Leu Asp His Val Val Glu Ile Leu Val Glu
225 230 235 240

Thr

<210> 5
<211> 106
<212> PRT
<213> Danio rerio

<400> 5

Met Phe Ser Lys Gly Thr Lys Arg Lys Phe Ala Asp Gly Gly Glu Glu

Met Phe Ala Arg Gly Leu Lys Arg Lys Cys Val Gly His Glu Glu Asp
 1 5 10 15

Val Glu Gly Ala Leu Ala Gly Leu Lys Thr Val Ser Ser Tyr Ser Leu
 20 25 30

Gln Arg Gln Ser Leu Leu Asp Met Ser Leu Val Lys Leu Gln Leu Cys
 35 40 45

His Met Leu Val Glu Pro Asn Leu Cys Arg Ser Val Leu Ile Ala Asn
 50 55 60

Thr Val Arg Gln Ile Gln Glu Glu Met Thr Gln Asp Gly Thr Trp Arg
 65 70 75 80

Thr Val Ala Pro Gln Ala Ala Glu Arg Ala Pro Leu Asp Arg Leu Val
 85 90 95

Ser Thr Glu Ile Leu Cys Arg Ala Ala Trp Gly Gln Glu Gly Ala His
 100 105 110

Pro Ala Pro Gly Leu
 115

<210> 8
 <211> 20
 <212> DNA
 <213> synthetic construct

<400> 8
 cgaaggagtg gcggggtctg 20

<210> 9
 <211> 20
 <212> DNA
 <213> synthetic construct

<400> 9
 ttcctttgcc ctctgtctga 20

<210> 10
 <211> 20
 <212> DNA
 <213> synthetic construct

<400> 10
 gttgagagat catctccacc 20

<210> 11
 <211> 20
 <212> DNA
 <213> synthetic construct

→

[illegible]